

SEQUENCE LISTING

<110> The Scripps Research Institute
The Regents of the University of California
Wu, Eugene
Nemerow, Glen R.
Stewart, Phoebe

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Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro	
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Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser	
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Leu	Arg	Val	Ser	Glu	Pro	Leu	Asp	Thr	Ser	His	Gly	Met	Leu	Ala	Leu	
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Gln	Asn	Val	Thr	Thr	Val	Thr	Gln	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn	
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ata	agt	ttg	gac	acc	tcc	gca	cca	ctt	aca	att	acc	tca	ggc	gcc	cta	336
Ile	Ser	Leu	Asp	Thr	Ser	Ala	Pro	Leu	Thr	Ile	Thr	Ser	Gly	Ala	Leu	
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225	230	235	240
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Gly Ala Ile Gly Tyr Asp Ser Ser Asn Asn Met Glu Ile Lys Thr Gly			
	245	250	255
ggt ggc atg cgt ata aat aac aac ttg tta att cta gat gtg gat tac			816
Gly Gly Met Arg Ile Asn Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr			
	260	265	270
cca ttt gat gct caa aca aaa cta cgt ctt aaa ctg ggg cag gga ccc			864
Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro			
	275	280	285
ctg tat att aat gca tct cat aac ttg gac ata aac tat aac aga ggc			912
Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly			
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Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser			
305	310	315	320
ata aaa aaa tcc agt gga cta aac ttt gat aat act gcc ata gct ata			1008
Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile			
	325	330	335
aat gca gga aag ggt ctg gag ttt gat aca aac aca tct gag tct cca			1056
Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro			
	340	345	350
gat atc aac cca ata aaa act aaa att ggc tct ggc att gat tac aat			1104
Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn			
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gaa aac ggt gcc atg att act aaa ctt gga gcg ggt tta agc ttt gac			1152
Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp			
	370	375	380
aac tca ggg gcc att aca ata gga aac aaa aat gat gac aaa ctt acc			1200
Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr			
385	390	395	400
ctg tgg aca acc cca gac cca tct cct aac tgc aga att cat tca gat			1248
Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp			
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Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val			
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Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met			
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Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe	
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Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly	
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Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala	
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Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu	
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Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu	
50 55 60	
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser	
65 70 75 80	
Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu	

			100						105						110					
Thr	Val	Ala	Thr	Thr	Ala	Pro	Leu	Ile	Val	Thr	Ser	Gly	Ala	Leu	Ser					
		115					120					125								
Val	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	Gln	Asp	Ser	Lys	Leu	Ser	Ile					
		130				135					140									
Ala	Thr	Lys	Gly	Pro	Ile	Thr	Val	Ser	Asp	Gly	Lys	Leu	Ala	Leu	Gln					
145					150					155					160					
Thr	Ser	Ala	Pro	Leu	Ser	Gly	Ser	Asp	Ser	Asp	Thr	Leu	Thr	Val	Thr					
				165					170					175						
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asn	Met					
			180					185					190							
Glu	Asp	Pro	Ile	Tyr	Val	Asn	Asn	Gly	Lys	Ile	Gly	Ile	Lys	Ile	Ser					
		195				200						205								
Gly	Pro	Leu	Gln	Val	Ala	Gln	Asn	Ser	Asp	Thr	Leu	Thr	Val	Val	Thr					
		210				215					220									
Gly	Pro	Gly	Val	Thr	Val	Glu	Gln	Asn	Ser	Leu	Arg	Thr	Lys	Val	Ala					
225					230					235					240					
Gly	Ala	Ile	Gly	Tyr	Asp	Ser	Ser	Asn	Asn	Met	Glu	Ile	Lys	Thr	Gly					
				245						250				255						
Gly	Gly	Met	Arg	Ile	Asn	Asn	Asn	Leu	Leu	Ile	Leu	Asp	Val	Asp	Tyr					
			260				265						270							
Pro	Phe	Asp	Ala	Gln	Thr	Lys	Leu	Arg	Leu	Lys	Leu	Gly	Gln	Gly	Pro					
		275					280					285								
Leu	Tyr	Ile	Asn	Ala	Ser	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn	Arg	Gly					
		290				295					300									
Leu	Tyr	Leu	Phe	Asn	Ala	Ser	Asn	Asn	Thr	Lys	Lys	Leu	Glu	Val	Ser					
305					310					315					320					
Ile	Lys	Lys	Ser	Ser	Gly	Leu	Asn	Phe	Asp	Thr	Asn	Thr	Ala	Ile	Ala	Ile				
				325					330					335						
Asn	Ala	Gly	Lys	Gly	Leu	Glu	Phe	Asp	Thr	Asn	Thr	Ser	Glu	Ser	Pro					
			340					345					350							
Asp	Ile	Asn	Pro	Ile	Lys	Thr	Lys	Ile	Gly	Ser	Gly	Ile	Asp	Tyr	Asn					
		355					360					365								
Glu	Asn	Gly	Ala	Met	Ile	Thr	Lys	Leu	Gly	Ala	Gly	Leu	Ser	Phe	Asp					
		370				375					380									
Asn	Ser	Gly	Ala	Ile	Thr	Ile	Gly	Asn	Lys	Asn	Asp	Asp	Lys	Leu	Thr					
385					390					395					400					
Leu	Trp	Thr	Thr	Pro	Asp	Pro	Ser	Pro	Asn	Cys	Arg	Ile	His	Ser	Asp					
				405					410					415						
Asn	Asp	Cys	Lys	Phe	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Val					
			420					425					430							
Leu	Ala	Thr	Val	Ala	Ala	Leu	Ala	Val	Ser	Gly	Asp	Leu	Ser	Ser	Met					
		435					440													

Ser Gly Lys Tyr Thr Thr Glu Thr Phe Ala Thr Asn Ser Tyr Thr Phe
565 570 575
Ser Tyr Ile Ala Gln Glu
580

<210> 34
<211> 1746
<212> DNA
<213> Adenovirus serotype 5 fiber

<220>
<221> CDS
<222> (1)...(1746)

<400> 34
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528

Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr		
				165					170					175			
gcc	tca	ccc	cct	cta	act	act	gcc	act	ggg	agc	ttg	ggc	att	gac	ttg	576	
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu		
			180					185					190				
aaa	gag	ccc	att	tat	aca	caa	aat	gga	aaa	cta	gga	cta	aag	tac	ggg	624	
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly		
		195					200					205					
gct	cct	ttg	cat	gta	aca	gac	gac	cta	aac	act	ttg	acc	gta	gca	act	672	
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr		
	210					215					220						
ggg	cca	ggg	gtg	act	att	aat	aat	act	tcc	ttg	caa	act	aaa	gtt	act	720	
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr		
225				230					235					240			
gga	gcc	ttg	ggg	ttt	gat	tca	caa	ggc	aat	atg	caa	ctt	aat	gta	gca	768	
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala		
			245					250						255			
gga	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata	ctt	gat	gtt	816	
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val		
		260						265				270					
agt	tat	ccg	ttt	gat	gct	caa	aac	caa	cta	aat	cta	aga	cta	gga	cag	864	
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln		
		275					280					285					
ggc	cct	ctt	ttt	ata	aac	tca	gcc	cac	aac	ttg	gat	att	aac	tac	aac	912	
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn		
	290					295					300						
aaa	ggc	ctt	tac	ttg	ttt	aca	gct	tca	aac	aat	tcc	aaa	aag	ctt	gag	960	
Lys	Gly	Leu	Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu		
305				310					315					320			
gtt	aac	cta	agc	act	gcc	aag	ggg	ttg	atg	ttt	gac	gct	aca	gcc	ata	1008	
Val	Asn	Leu	Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr	Ala	Ile		
				325				330					335				
gcc	att	aat	gca	gga	gat	ggg	ctt	gaa	ttt	ggg	tca	cct	aat	gca	cca	1056	
Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro		
			340					345					350				
aac	aca	aat	ccc	ctc	aaa	aca	aaa	att	ggc	cat	ggc	cta	gaa	ttt	gat	1104	
Asn	Thr	Asn	Pro	Leu	Lys	Thr	Lys	Ile	Gly	His	Gly	Leu	Glu	Phe	Asp		
		355					360					365					
tca	aac	aag	gct	atg	gtt	cct	aaa	cta	gga	act	ggc	ctt	agt	ttt	gac	1152	
Ser	Asn	Lys	Ala	Met	Val	Pro	Lys	Leu	Gly	Thr	Gly	Leu	Ser	Phe	Asp		
	370					375					380						
agc	aca	ggg	gcc	att	aca	gta	gga	aac	aaa	aat	aat	gat	aag	cta	act	1200	
Ser	Thr	Gly	Ala	Ile	Thr	Val	Gly	Asn	Lys	Asn	Asn	Asp	Lys	Leu	Thr		

385	390	395	400	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag				1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu				
	405	410	415	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata				1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile				
	420	425	430	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata				1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile				
	435	440	445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat				1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn				
	450	455	460	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt				1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe				
	465	470	475	480
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga				1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly				
	485	490	495	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc				1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala				
	500	505	510	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa				1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys				
	515	520	525	
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac				1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp				
	530	535	540	
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc				1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly				
	545	550	555	560
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca				1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser				
	565	570	575	
tac att gcc caa gaa taa				1746
Tyr Ile Ala Gln Glu *				
	580			

<210> 35

<211> 581

<212> PRT

<213> Adenovirus serotype 5 fiber

<400> 35

Met	Lys	Arg	Ala	Arg	Pro	Ser	Glu	Asp	Thr	Phe	Asn	Pro	Val	Tyr	Pro	
1				5					10					15		
Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro	
			20					25					30			
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser	
		35				40						45				
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu	
	50					55					60					
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser	
65					70					75					80	
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn	
				85					90						95	
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu	
			100					105					110			
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr	
		115					120					125				
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile	
	130					135					140					
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln	
145					150					155					160	
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr	
				165					170					175		
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu	
			180					185					190			
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly	
	195					200						205				
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr	
	210					215					220					
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr	
225					230						235				240	
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala	
				245					250					255		
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val	
			260					265					270			
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln	
		275				280						285				
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn	
	290					295					300					
Lys	Gly	Leu	Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu	
305					310					315					320	
Val	Asn	Leu	Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr	Ala	Ile	
				325					330					335		
Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro	
			340					345					350			
Asn	Thr	Asn	Pro	Leu	Lys	Thr	Lys	Ile	Gly	His	Gly	Leu	Glu	Phe	Asp	
	355						360					365				
Ser	Asn	Lys	Ala	Met	Val	Pro	Lys	Leu	Gly	Thr	Gly	Leu	Ser	Phe	Asp	
	370					375					380					
Ser	Thr	Gly	Ala	Ile	Thr	Val	Gly	Asn	Lys	Asn	Asn	Asp	Lys	Leu	Thr	
385					390					395					400	
Leu	Trp	Thr	Thr	Pro	Ala	Pro	Ser	Pro	Asn	Cys	Arg	Leu	Asn	Ala	Glu	
				405					410					415		
Lys	Asp	Ala	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	
		420						425				430				
Leu	Ala	Thr	Val	Ser	Val	Leu	Ala	Val	Lys	Gly	Ser	Leu	Ala	Pro	Ile	
	435					440					445					
Ser	Gly	Thr	Val	Gln	Ser	Ala	His	Leu	Ile	Ile	Arg	Phe	Asp	Glu	Asn	

450		455		460
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe				
465		470		475
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly				480
	485		490	495
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala				
	500		505	510
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys				
	515		520	525
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp				
	530		535	540
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly				
545		550		555
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser				560
	565		570	575
Tyr Ile Ala Gln Glu				
	580			

<210> 36
 <211> 1098
 <212> DNA
 <213> Adenovirus serotype 37 fiber

<220>
 <221> CDS
 <222> (1)...(1098)

<400> 36	
atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc	48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro	
1 5 10 15	
tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt	96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe	
20 25 30	
gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc	144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
35 40 45	
aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag	192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
50 55 60	
gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct	240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
65 70 75 80	
aag gct cca ctg caa gtt aat act gat aaa aaa ctt gag ctt gca tat	288
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
85 90 95	
gat aat cca ttt gaa agt agt gct aat aaa ctt agt tta aaa gta gga	336
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly	
100 105 110	

cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat	384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa	432
Leu Ile Gly Lys Leu Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta	480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca	528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca	576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr	
180 185 190	
tct cca aac tgc aca att gct caa gat aag gac tct aaa ctc act ttg	624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	
195 200 205	
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att	672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile	
210 215 220	
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca aaa	720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys	
225 230 235 240	
ata aaa agt ttt act att aaa ctg cta ttt aat aag aac gga gtg ctt	768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu	
245 250 255	
tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga	816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly	
260 265 270	
aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct	864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro	
275 280 285	
aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga	912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg	
290 295 300	
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca	960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro	
305 310 315 320	
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct	1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser	
325 330 335	
atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt	1056

Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
 340 345 350

gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga
 Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *
 355 360 365

1098

<210> 37
 <211> 365
 <212> PRT
 <213> Adenovirus serotype 37 fiber

<400> 37
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
 50 55 60
 Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
 65 70 75 80
 Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
 85 90 95
 Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
 100 105 110
 His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
 115 120 125
 Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
 130 135 140
 Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
 145 150 155 160
 Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
 165 170 175
 Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
 180 185 190
 Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
 195 200 205
 Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
 210 215 220
 Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys
 225 230 235 240
 Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
 245 250 255
 Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
 260 265 270
 Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
 275 280 285
 Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
 290 295 300
 Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
 305 310 315 320
 Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
 325 330 335

Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
 340 345 350
 Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
 355 360 365

<210> 38
 <211> 1098
 <212> DNA
 <213> Adenovirus serotype 19p fiber

<220>
 <221> CDS
 <222> (1)...(1098)

<400> 38
 atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc 48
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt 96
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc 144
 Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag 192
 Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
 50 55 60

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct 240
 Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
 65 70 75 80

aag gct cca ctg caa gtt act act gat aaa aaa ctt gag ctt gca tat 288
 Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
 85 90 95

gat aat cca ttt gaa tgt agt gct aat aaa ttt agt tta aaa gta gga 336
 Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
 100 105 110

cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat 384
 His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
 115 120 125

tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa 432
 Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
 130 135 140

aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta 480
 Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
 145 150 155 160

aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca 528

Arg	Ala	Arg	Glu	Gly	Leu	Thr	Phe	Asp	Asn	Asp	Gly	Tyr	Leu	Val	Ala	
			165						170					175		
tgg	aac	cca	aag	tat	gac	acg	cgc	aca	ctt	tgg	aca	aca	cca	gac	aca	576
Trp	Asn	Pro	Lys	Tyr	Asp	Thr	Arg	Thr	Leu	Trp	Thr	Thr	Pro	Asp	Thr	
			180					185					190			
tct	cca	aac	tgc	aca	att	gct	cag	gat	aag	gac	tct	aaa	ctc	act	ttg	624
Ser	Pro	Asn	Cys	Thr	Ile	Ala	Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu	
			195				200					205				
gta	ctt	aca	aag	tgt	gga	agt	caa	ata	tta	gct	aat	gtg	tct	ttg	att	672
Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	
	210					215				220						
gtg	gtc	gca	gga	aag	tac	cac	atc	ata	aat	aat	aag	aca	aat	cca	gaa	720
Val	Val	Ala	Gly	Lys	Tyr	His	Ile	Ile	Asn	Asn	Lys	Thr	Asn	Pro	Glu	
225					230				235					240		
ata	aaa	agt	ttt	act	att	aaa	ctg	tta	ttt	aat	aag	aac	gga	gtg	ctt	768
Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu	Phe	Asn	Lys	Asn	Gly	Val	Leu	
			245					250					255			
tta	gac	aac	tca	aat	ctt	gga	aaa	gct	tat	tgg	aac	ttt	aga	agt	gga	816
Leu	Asp	Asn	Ser	Asn	Leu	Gly	Lys	Ala	Tyr	Trp	Asn	Phe	Arg	Ser	Gly	
			260					265					270			
aat	tcc	aat	gtt	tcg	aca	gct	tat	gaa	aaa	gca	att	ggt	ttt	atg	cct	864
Asn	Ser	Asn	Val	Ser	Thr	Ala	Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro	
			275				280					285				
aat	tta	gta	gcg	tat	cca	aaa	ccc	agt	aat	tct	aaa	aaa	tat	gca	aga	912
Asn	Leu	Val	Ala	Tyr	Pro	Lys	Pro	Ser	Asn	Ser	Lys	Lys	Tyr	Ala	Arg	
	290					295					300					
gac	ata	gtt	tat	gga	act	ata	tat	ctt	ggt	gga	aaa	cct	gat	cag	cca	960
Asp	Ile	Val	Tyr	Gly	Thr	Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro	
305					310				315					320		
gca	gtc	att	aaa	act	acc	ttt	aac	caa	gaa	act	gga	tgt	gaa	tac	tct	1008
Ala	Val	Ile	Lys	Thr	Thr	Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser	
				325				330					335			
atc	aca	ttt	gac	ttt	agt	tgg	tcc	aaa	acc	tat	gaa	aat	gtt	gaa	ttt	1056
Ile	Thr	Phe	Asp	Phe	Ser	Trp	Ser	Lys	Thr	Tyr	Glu	Asn	Val	Glu	Phe	
			340					345					350			
gaa	acc	acc	tct	ttt	acc	ttc	tcc	tat	att	gcc	caa	gaa	tga			1098
Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu	*			
			355				360					365				

<210> 39

<211> 365

<212> PRT

<213> Adenovirus serotype 19p fiber

<400> 39

Met	Ser	Lys	Arg	Leu	Arg	Val	Glu	Asp	Asp	Phe	Asn	Pro	Val	Tyr	Pro	
1				5					10					15		
Tyr	Gly	Tyr	Ala	Arg	Asn	Gln	Asn	Ile	Pro	Phe	Leu	Thr	Pro	Pro	Phe	
			20					25					30			
Val	Ser	Ser	Asp	Gly	Phe	Lys	Asn	Phe	Pro	Pro	Gly	Val	Leu	Ser	Leu	
		35					40					45				
Lys	Leu	Ala	Asp	Pro	Ile	Thr	Ile	Thr	Asn	Gly	Asp	Val	Ser	Leu	Lys	
	50					55					60					
Val	Gly	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Ser	Leu	Thr	Val	Asn	Pro	
65					70					75					80	
Lys	Ala	Pro	Leu	Gln	Val	Thr	Thr	Asp	Lys	Lys	Leu	Glu	Leu	Ala	Tyr	
				85					90					95		
Asp	Asn	Pro	Phe	Glu	Cys	Ser	Ala	Asn	Lys	Phe	Ser	Leu	Lys	Val	Gly	
			100					105					110			
His	Gly	Leu	Lys	Val	Leu	Asp	Glu	Lys	Ser	Ala	Ala	Gly	Leu	Lys	Asp	
	115						120					125				
Leu	Ile	Gly	Lys	Leu	Val	Val	Leu	Thr	Gly	Lys	Gly	Ile	Gly	Thr	Glu	
	130					135					140					
Asn	Leu	Glu	Asn	Thr	Asp	Gly	Ser	Ser	Arg	Gly	Ile	Gly	Ile	Asn	Val	
145				150					155					160		
Arg	Ala	Arg	Glu	Gly	Leu	Thr	Phe	Asp	Asn	Asp	Gly	Tyr	Leu	Val	Ala	
			165						170					175		
Trp	Asn	Pro	Lys	Tyr	Asp	Thr	Arg	Thr	Leu	Trp	Thr	Thr	Pro	Asp	Thr	
		180						185					190			
Ser	Pro	Asn	Cys	Thr	Ile	Ala	Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu	
		195				200						205				
Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	
	210					215					220					
Val	Val	Ala	Gly	Lys	Tyr	His	Ile	Ile	Asn	Asn	Lys	Thr	Asn	Pro	Glu	
225				230						235				240		
Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu	Phe	Asn	Lys	Asn	Gly	Val	Leu	
			245						250				255			
Leu	Asp	Asn	Ser	Asn	Leu	Gly	Lys	Ala	Tyr	Trp	Asn	Phe	Arg	Ser	Gly	
		260				265						270				
Asn	Ser	Asn	Val	Ser	Thr	Ala	Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro	
		275				280						285				
Asn	Leu	Val	Ala	Tyr	Pro	Lys	Pro	Ser	Asn	Ser	Lys	Lys	Tyr	Ala	Arg	
	290					295					300					
Asp	Ile	Val	Tyr	Gly	Thr	Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro	
305				310						315				320		
Ala	Val	Ile	Lys	Thr	Thr	Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser	
			325						330				335			
Ile	Thr	Phe	Asp	Phe	Ser	Trp	Ser	Lys	Thr	Tyr	Glu	Asn	Val	Glu	Phe	
			340					345					350			
Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu				
		355					360					365				

<210> 40

<211> 1228

<212> DNA

<213> Adenovirus serotype 9 fiber

<220>

<221> CDS

<222> (50)...(1138)

<400> 40

aagggatgtc aaattcctgg tccacaattt tcattgtctt ccctctcag atg tca aag 58
Met Ser Lys
1

agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat ggc tac 106
Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr
5 10 15

gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc 154
Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser
20 25 30 35

gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct 202
Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala
40 45 50

gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtg gga ggg 250
Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly
55 60 65

ggt ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat 298
Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp
70 75 80

cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct 346
Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala
85 90 95

cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc 394
Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly
100 105 110 115

ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat 442
Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn
120 125 130

act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat 490
Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp
135 140 145

aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca 538
Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Gly Leu Ser
150 155 160

ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag 586
Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys
165 170 175

cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat 634
Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp
180 185 190 195

cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt 682
Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser

200										205					210					
caa	ata	ttg	gct	aat	gtg	tca	tta	att	gtc	gta	gat	ggt	aag	tac	aaa	730				
Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	Val	Val	Asp	Gly	Lys	Tyr	Lys					
			215				220						225							
att	atc	aat	aac	aat	act	caa	cca	gct	ctc	aaa	gga	ttt	acc	att	aaa	778				
Ile	Ile	Asn	Asn	Asn	Thr	Gln	Pro	Ala	Leu	Lys	Gly	Phe	Thr	Ile	Lys					
			230				235						240							
tta	ttg	ttt	gat	gaa	aat	gga	gta	ctt	atg	gaa	tct	tca	aat	ctt	ggt	826				
Leu	Leu	Phe	Asp	Glu	Asn	Gly	Val	Leu	Met	Glu	Ser	Ser	Asn	Leu	Gly					
			245				250						255							
aaa	tca	tat	tgg	aac	ttt	aga	aat	gaa	aat	tca	att	atg	tca	aca	gct	874				
Lys	Ser	Tyr	Trp	Asn	Phe	Arg	Asn	Glu	Asn	Ser	Ile	Met	Ser	Thr	Ala					
260						265						270			275					
tat	gaa	aaa	gct	att	gga	ttc	atg	cct	aat	ttg	gta	gcc	tat	cca	aaa	922				
Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro	Asn	Leu	Val	Ala	Tyr	Pro	Lys					
			280						285						290					
cct	acc	gct	ggc	tct	aaa	aaa	tat	gca	aga	gat	ata	gtt	tat	gga	aac	970				
Pro	Thr	Ala	Gly	Ser	Lys	Lys	Tyr	Ala	Arg	Asp	Ile	Val	Tyr	Gly	Asn					
			295						300						305					
atc	tac	ctt	ggt	gga	aag	cca	gat	caa	cca	gta	acc	att	aaa	act	acc	1018				
Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro	Val	Thr	Ile	Lys	Thr	Thr					
			310						315						320					
ttt	aat	cag	gaa	act	gga	tgt	gaa	tat	tct	atc	aca	ttt	gat	ttt	agt	1066				
Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	Phe	Asp	Phe	Ser					
			325						330						335					
tgg	gcc	aag	act	tat	gta	aat	gtt	gaa	ttt	gaa	aca	acc	tct	ttt	acc	1114				
Trp	Ala	Lys	Thr	Tyr	Val	Asn	Val	Glu	Phe	Glu	Thr	Thr	Ser	Phe	Thr					
340						345						350			355					
ttt	tcc	tat	atc	gcc	caa	gaa	tga	aagaccaata	aacgtgtttt	tcattttcaaa	1168									
Phe	Ser	Tyr	Ile	Ala	Gln	Glu	*													
			360																	

attttcatgt atctttattg atttttacac cagcacgggt agtcagtctc ccaccaccag 1228

<210> 41
 <211> 362
 <212> PRT
 <213> Adenovirus serotype 9 fiber

<400> 41
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45

Lys	Leu	Ala	Asp	Pro	Ile	Ala	Ile	Val	Asn	Gly	Asn	Val	Ser	Leu	Lys	50	55	60
Val	Gly	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Thr	Gly	Lys	Leu	Thr	Val	65	70	75
Asn	Ala	Asp	Pro	Pro	Leu	Gln	Leu	Thr	Asn	Asn	Lys	Leu	Gly	Ile	Ala	85	90	95
Leu	Asp	Ala	Pro	Phe	Asp	Val	Ile	Asp	Asn	Lys	Leu	Thr	Leu	Leu	Ala	100	105	110
Gly	His	Gly	Leu	Ser	Ile	Ile	Thr	Lys	Glu	Thr	Ser	Thr	Leu	Pro	Gly	115	120	125
Leu	Arg	Asn	Thr	Leu	Val	Val	Leu	Thr	Gly	Lys	Gly	Ile	Gly	Thr	Glu	130	135	140
Ser	Thr	Asp	Asn	Gly	Gly	Thr	Val	Cys	Val	Arg	Val	Gly	Glu	Gly	Gly	145	150	155
Gly	Leu	Ser	Phe	Asn	Asn	Asp	Gly	Asp	Leu	Val	Ala	Phe	Asn	Lys	Lys	165	170	175
Glu	Asp	Lys	Arg	Thr	Leu	Trp	Thr	Thr	Pro	Asp	Thr	Ser	Pro	Asn	Cys	180	185	190
Lys	Ile	Asp	Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	195	200	205
Cys	Gly	Ser	Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	Val	Val	Asp	Gly	210	215	220
Lys	Tyr	Lys	Ile	Ile	Asn	Asn	Asn	Thr	Gln	Pro	Ala	Leu	Lys	Gly	Phe	225	230	235
Thr	Ile	Lys	Leu	Leu	Phe	Asp	Glu	Asn	Gly	Val	Leu	Met	Glu	Ser	Ser	245	250	255
Asn	Leu	Gly	Lys	Ser	Tyr	Trp	Asn	Phe	Arg	Asn	Glu	Asn	Ser	Ile	Met	260	265	270
Ser	Thr	Ala	Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro	Asn	Leu	Val	Ala	275	280	285
Tyr	Pro	Lys	Pro	Thr	Ala	Gly	Ser	Lys	Lys	Tyr	Ala	Arg	Asp	Ile	Val	290	295	300
Tyr	Gly	Asn	Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro	Val	Thr	Ile	305	310	315
Lys	Thr	Thr	Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	Phe	325	330	335
Asp	Phe	Ser	Trp	Ala	Lys	Thr	Tyr	Val	Asn	Val	Glu	Phe	Glu	Thr	Thr	340	345	350
Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu							355	360	

<210> 42

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad2 third repeat

<400> 42

Gly	Asn	Leu	Thr	Ser	Gln	Asn	Val	Thr	Thr	Val	Thr	Gln	Pro	Leu	Lys	1	5	10	15
Lys	Thr	Lys	Ser													20			

<210> 46
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2 21st repeat

<400> 46
Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser
1 5 10 15

<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 21st repeat

<400> 47
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr
1 5 10 15

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 last repeat

<400> 48
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp
1 5 10 15

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Last repeat consensus sequence

<221> VARIANT
<222> 4,7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 9
<223> Xaa = Asp or Asn

<400> 49
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa

1

5

<210> 50
 <211> 1164
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5Ds fiber

<221> CDS
 <222> (13)...(1092)

<221> misc_feature
 <222> 1130, 1157
 <223> n = A,T,C or G

<400> 50

atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro

1

5

10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30 35 40 45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
 50 55 60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac 243
 Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
 65 70 75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc 291
 Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
 80 85 90

aag aaa aag ctt gaa gtt aac cta agc act gcc aag ggg ttg atg ttt 339
 Lys Lys Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe
 95 100 105

gac gct aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt 387
 Asp Ala Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly
 110 115 120 125

tca cct aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat 435
 Ser Pro Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His
 130 135 140

ggc cta gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act 483
 Gly Leu Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr

145	150	155	
ggc ctt agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat			531
Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn			
160	165	170	
aat gat aag cta act ttg tgg acc aca cca gct cca tct cct aac tgt			579
Asn Asp Lys Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys			
175	180	185	
aga cta aat gca gag aaa gat gct aaa ctc act ttg gtc tta aca aaa			627
Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys			
190	195	200	205
tgt ggc agt caa ata ctt gct aca gtt tca gtt ttg gct gtt aaa ggc			675
Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly			
210	215	220	
agt ttg gct cca ata tct gga aca gtt caa agt gct cat ctt att ata			723
Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile			
225	230	235	
aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca			771
Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro			
240	245	250	
gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat			819
Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr			
255	260	265	
aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct			867
Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser			
270	275	280	285
cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac			915
His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn			
290	295	300	
gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca			963
Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr			
305	310	315	
cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca			1011
Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser			
320	325	330	
tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc			1059
Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser			
335	340	345	
tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcgttatgaa			1112
Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu *			
350	355		
gggcgaattc cagcacantg gcggccgtta ttagtggatc cgagntcatg ca			1164

<211> 359
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad5deltas

<400> 51

Met	Lys	Arg	Ala	Arg	Pro	Ser	Glu	Asp	Thr	Phe	Asn	Pro	Val	Tyr	Pro
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Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro
			20					25					30		
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser
		35					40					45			
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu
	50					55					60				
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser
65					70					75				80	
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Lys	Lys
				85					90					95	
Leu	Glu	Val	Asn	Leu	Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr
			100					105					110		
Ala	Ile	Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn
	115						120					125			
Ala	Pro	Asn	Thr	Asn	Pro	Leu	Lys	Thr	Lys	Ile	Gly	His	Gly	Leu	Glu
	130					135					140				
Phe	Asp	Ser	Asn	Lys	Ala	Met	Val	Pro	Lys	Leu	Gly	Thr	Gly	Leu	Ser
145					150					155					160
Phe	Asp	Ser	Thr	Gly	Ala	Ile	Thr	Val	Gly	Asn	Lys	Asn	Asn	Asp	Lys
				165					170					175	
Leu	Thr	Leu	Trp	Thr	Thr	Pro	Ala	Pro	Ser	Pro	Asn	Cys	Arg	Leu	Asn
			180					185					190		
Ala	Glu	Lys	Asp	Ala	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser
	195						200					205			
Gln	Ile	Leu	Ala	Thr	Val	Ser	Val	Leu	Ala	Val	Lys	Gly	Ser	Leu	Ala
	210					215					220				
Pro	Ile	Ser	Gly	Thr	Val	Gln	Ser	Ala	His	Leu	Ile	Ile	Arg	Phe	Asp
225					230					235				240	
Glu	Asn	Gly	Val	Leu	Leu	Asn	Asn	Ser	Phe	Leu	Asp	Pro	Glu	Tyr	Trp
			245						250					255	
Asn	Phe	Arg	Asn	Gly	Asp	Leu	Thr	Glu	Gly	Thr	Ala	Tyr	Thr	Asn	Ala
		260						265					270		
Val	Gly	Phe	Met	Pro	Asn	Leu	Ser	Ala	Tyr	Pro	Lys	Ser	His	Gly	Lys
	275						280					285			
Thr	Ala	Lys	Ser	Asn	Ile	Val	Ser	Gln	Val	Tyr	Leu	Asn	Gly	Asp	Lys
	290					295					300				
Thr	Lys	Pro	Val	Thr	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Gln	Glu	Thr
305					310					315					320
Gly	Asp	Thr	Thr	Pro	Ser	Ala	Tyr	Ser	Met	Ser	Phe	Ser	Trp	Asp	Trp
				325					330					335	
Ser	Gly	His	Asn	Tyr	Ile	Asn	Glu	Ile	Phe	Ala	Thr	Ser	Ser	Tyr	Thr
			340					345					350		
Phe	Ser	Tyr	Ile	Ala	Gln	Glu									
			355												

<210> 52

<211> 1920
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37k fiber

<221> CDS
 <222> (13)...(1755)

<221> misc_feature
 <222> 1867, 1875
 <223> n = A,T,C or G

<400> 52

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gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
      Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
            1              5              10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
      15              20              25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
      30              35              40              45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
            50              55              60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac 243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
            65              70              75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc 291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
            80              85              90

aag tca aac ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca 339
Lys Ser Asn Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser
            95              100             105

gaa gcc cta act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac 387
Glu Ala Leu Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn
      110              115              120              125

aca ctc acc atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa 435
Thr Leu Thr Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys
            130              135              140

ctt agc att gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta 483
Leu Ser Ile Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu
            145              150              155

gcc ctg caa aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt 531
Ala Leu Gln Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu

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160	165	170	
act atc act gcc tca ccc cct cta act act gcc act ggt agc ttg ggc Thr Ile Thr Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly 175 180 185			579
att gac ttg aaa gag ccc att tat aca caa aat gga aaa cta gga cta Ile Asp Leu Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu 190 195 200 205			627
aag tac ggg gct cct ttg cat gta aca gac gac cta aac act ttg acc Lys Tyr Gly Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr 210 215 220			675
gta gca act ggt cca ggt gtg act att aat aat act tcc ttg caa act Val Ala Thr Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr 225 230 235			723
aaa gtt act gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt Lys Val Thr Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu 240 245 250			771
aat gta gca gga gga cta agg att gat tct caa aac aga cgc ctt ata Asn Val Ala Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile 255 260 265			819
ctt gat gtt agt tat ccg ttt gat gct caa aac caa cta aat cta aga Leu Asp Val Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg 270 275 280 285			867
cta gga cag ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att Leu Gly Gln Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile 290 295 300			915
aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys 305 310 315			963
aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala 320 325 330			1011
aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro 335 340 345			1059
aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu 350 355 360 365			1107
gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu 370 375 380			1155
agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp 385 390 395			1203

aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att	1251
Lys Leu Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile	
400 405 410	
gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga	1299
Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly	
415 420 425	
agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac	1347
Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr	
430 435 440 445	
cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att	1395
His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile	
450 455 460	
aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt	1443
Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu	
465 470 475	
gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca	1491
Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr	
480 485 490	
gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca	1539
Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro	
495 500 505	
aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act	1587
Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr	
510 515 520 525	
ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc	1635
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr	
530 535 540	
ttt aac caa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt	1683
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser	
545 550 555	
tgg tcc aaa acc tat gaa aat gtt gaa ttt gaa acc acc tct ttt acc	1731
Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr	
560 565 570	
ttc tcc tat att gcc caa gaa tga aaaagcggcc gctcgagtct agagggcccg	1785
Phe Ser Tyr Ile Ala Gln Glu *	
575 580	
tttaaaccgg ctgatcagcc tcgactgtgc cttctagttg ccagccatct gttgtttgcc	1845
cctccccgt gccttccttg ancctggaan gtgccactcc cactgtcctt tcctaataaa	1905
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<210> 53

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad5s/Ad37k

<400> 53

Met	Lys	Arg	Ala	Arg	Pro	Ser	Glu	Asp	Thr	Phe	Asn	Pro	Val	Tyr	Pro
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Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro
			20					25					30		
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser
			35				40					45			
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu
	50					55					60				
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser
65					70					75				80	
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn
				85					90					95	
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu
			100					105					110		
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr
		115					120					125			
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile
	130					135					140				
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln
145					150					155				160	
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr
				165					170					175	
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu
			180					185					190		
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly
		195					200					205			
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr
	210					215					220				
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr
225					230					235				240	
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala
				245					250					255	
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val
			260					265					270		
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln
	275					280						285			
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn
	290				295						300				
Lys	Gly	Leu	Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu
305					310					315				320	
Val	Asn	Leu	Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr	Ala	Ile
				325					330					335	
Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro
			340					345					350		
Asn	Thr	Asn	Pro	Leu	Lys	Thr	Lys	Ile	Gly	His	Gly	Leu	Glu	Phe	Asp
		355					360					365			
Ser	Asn	Lys	Ala	Met	Val	Pro	Lys	Leu	Gly	Thr	Gly	Leu	Ser	Phe	Asp
	370					375					380				
Ser	Thr	Gly	Ala	Ile	Thr	Val	Gly	Asn	Lys	Asn	Asn	Asp	Lys	Leu	Thr
385					390					395				400	
Leu	Trp	Thr	Thr	Pro	Asp	Thr	Ser	Pro	Asn	Cys	Thr	Ile	Ala	Gln	Asp
				405					410					415	

Lys	Asp	Ser	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile
			420					425					430		
Leu	Ala	Asn	Val	Ser	Leu	Ile	Val	Val	Ala	Gly	Lys	Tyr	His	Ile	Ile
		435					440					445			
Asn	Asn	Lys	Thr	Asn	Pro	Lys	Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu
	450					455					460				
Phe	Asn	Lys	Asn	Gly	Val	Leu	Leu	Asp	Asn	Ser	Asn	Leu	Gly	Lys	Ala
465					470					475					480
Tyr	Trp	Asn	Phe	Arg	Ser	Gly	Asn	Ser	Asn	Val	Ser	Thr	Ala	Tyr	Glu
				485					490						495
Lys	Ala	Ile	Gly	Phe	Met	Pro	Asn	Leu	Val	Ala	Tyr	Pro	Lys	Pro	Ser
			500					505					510		
Asn	Ser	Lys	Lys	Tyr	Ala	Arg	Asp	Ile	Val	Tyr	Gly	Thr	Ile	Tyr	Leu
		515					520					525			
Gly	Gly	Lys	Pro	Asp	Gln	Pro	Ala	Val	Ile	Lys	Thr	Thr	Phe	Asn	Gln
	530					535					540				
Glu	Thr	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	Phe	Asn	Phe	Ser	Trp	Ser	Lys
545					550					555					560
Thr	Tyr	Glu	Asn	Val	Glu	Phe	Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr
				565					570						575
Ile	Ala	Gln	Glu												
			580												

<210> 54
 <211> 1767
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37s fiber

<221> CDS
 <222> (13)...(1749)

<400> 54
 atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30 35 40 45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
 50 55 60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc agc 243
 Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser
 65 70 75

cta act gta aac cct aag gct cca ctg caa gtt aat act gat tca aac 291

Leu	Thr	Val	Asn	Pro	Lys	Ala	Pro	Leu	Gln	Val	Asn	Thr	Asp	Ser	Asn		
		80					85					90					
ata	aac	ctg	gaa	ata	tct	gca	ccc	ctc	aca	gtt	acc	tca	gaa	gcc	cta	339	
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu		
	95					100					105						
act	gtg	gct	gcc	gcc	gca	cct	cta	atg	gtc	gcg	ggc	aac	aca	ctc	acc	387	
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr		
110					115					120					125		
atg	caa	tca	cag	gcc	ccg	cta	acc	gtg	cac	gac	tcc	aaa	ctt	agc	att	435	
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile		
				130					135						140		
gcc	acc	caa	gga	ccc	ctc	aca	gtg	tca	gaa	gga	aag	cta	gcc	ctg	caa	483	
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln		
			145					150					155				
aca	tca	ggc	ccc	ctc	acc	acc	acc	gat	agc	agt	acc	ctt	act	atc	act	531	
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr		
		160					165					170					
gcc	tca	ccc	cct	cta	act	act	gcc	act	ggt	agc	ttg	ggc	att	gac	ttg	579	
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu		
	175					180					185						
aaa	gag	ccc	att	tat	aca	caa	aat	gga	aaa	cta	gga	cta	aag	tac	ggg	627	
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly		
190					195					200					205		
gct	cct	ttg	cat	gta	aca	gac	gac	cta	aac	act	ttg	acc	gta	gca	act	675	
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr		
				210					215					220			
ggt	cca	ggt	gtg	act	att	aat	aat	act	tcc	ttg	caa	act	aaa	ggt	act	723	
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr		
			225					230					235				
gga	gcc	ttg	ggt	ttt	gat	tca	caa	ggc	aat	atg	caa	ctt	aat	gta	gca	771	
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala		
		240					245					250					
gga	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata	ctt	gat	ggt	819	
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val		
		255					260				265						
agt	tat	ccg	ttt	gat	gct	caa	aac	caa	cta	aat	cta	aga	cta	gga	cag	867	
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln		
270					275					280					285		
ggc	cct	ctt	ttt	ata	aac	tca	gcc	cac	aac	ttg	gat	att	aac	tac	aac	915	
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn		
				290					295					300			
aaa	ggc	ctt	tac	ttg	ttt	aca	gct	tca	aac	aat	tcc	aaa	aag	ctt	gag	963	
Lys	Gly	Leu	Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu		

305					310					315						
ggt	aac	cta	agc	act	gcc	aag	ggg	ttg	atg	ttt	gac	gct	aca	gcc	ata	1011
Val	Asn	Leu	Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr	Ala	Ile	
		320					325					330				
gcc	att	aat	gca	gga	gat	ggg	ctt	gaa	ttt	ggg	tca	cct	aat	gca	cca	1059
Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro	
	335					340					345					
aac	aca	aat	ccc	ctc	aaa	aca	aaa	att	ggc	cat	ggc	cta	gaa	ttt	gat	1107
Asn	Thr	Asn	Pro	Leu	Lys	Thr	Lys	Ile	Gly	His	Gly	Leu	Glu	Phe	Asp	
350					355					360					365	
tca	aac	att	ggg	ata	aat	gta	aga	gca	aga	gaa	ggg	ttg	aca	ttt	gac	1155
Ser	Asn	Ile	Gly	Ile	Asn	Val	Arg	Ala	Arg	Glu	Gly	Leu	Thr	Phe	Asp	
				370					375						380	
aat	gat	ggg	gcc	att	aca	gta	gga	aac	aaa	aat	aat	gat	aag	cta	act	1203
Asn	Asp	Gly	Ala	Ile	Thr	Val	Gly	Asn	Lys	Asn	Asn	Asp	Lys	Leu	Thr	
			385					390					395			
ttg	tgg	acc	aca	cca	gct	cca	tct	cct	aac	tgt	aga	cta	aat	gca	gag	1251
Leu	Trp	Thr	Thr	Pro	Ala	Pro	Ser	Pro	Asn	Cys	Arg	Leu	Asn	Ala	Glu	
		400					405					410				
aaa	gat	gct	aaa	ctc	act	ttg	gtc	tta	aca	aaa	tgt	ggc	agt	caa	ata	1299
Lys	Asp	Ala	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	
	415					420					425					
ctt	gct	aca	ggt	tca	ggt	ttg	gct	ggt	aaa	ggc	agt	ttg	gct	cca	ata	1347
Leu	Ala	Thr	Val	Ser	Val	Leu	Ala	Val	Lys	Gly	Ser	Leu	Ala	Pro	Ile	
430					435					440					445	
tct	gga	aca	ggt	caa	agt	gct	cat	ctt	att	ata	aga	ttt	gac	gaa	aat	1395
Ser	Gly	Thr	Val	Gln	Ser	Ala	His	Leu	Ile	Ile	Arg	Phe	Asp	Glu	Asn	
				450					455						460	
gga	gtg	cta	cta	aac	aat	tcc	ttc	ctg	gac	cca	gaa	tat	tgg	aac	ttt	1443
Gly	Val	Leu	Leu	Asn	Asn	Ser	Phe	Leu	Asp	Pro	Glu	Tyr	Trp	Asn	Phe	
			465					470					475			
aga	aat	gga	gat	ctt	act	gaa	ggc	aca	gcc	tat	aca	aac	gct	ggt	gga	1491
Arg	Asn	Gly	Asp	Leu	Thr	Glu	Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly	
		480					485					490				
ttt	atg	cct	aac	cta	tca	gct	tat	cca	aaa	tct	cac	ggg	aaa	act	gcc	1539
Phe	Met	Pro	Asn	Leu	Ser	Ala	Tyr	Pro	Lys	Ser	His	Gly	Lys	Thr	Ala	
	495					500					505					
aaa	agt	aac	att	gtc	agt	caa	ggt	tac	tta	aac	gga	gac	aaa	act	aaa	1587
Lys	Ser	Asn	Ile	Val	Ser	Gln	Val	Tyr	Leu	Asn	Gly	Asp	Lys	Thr	Lys	
510					515					520					525	
cct	gta	aca	cta	acc	att	aca	cta	aac	ggg	aca	cag	gaa	aca	gga	gac	1635
Pro	Val	Thr	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Gln	Glu	Thr	Gly	Asp	
				530					535						540	

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1683
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
 545 550 555

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 1731
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
 560 565 570

tac att gcc caa gaa taa agaagcggcc gcgttatg 1767
 Tyr Ile Ala Gln Glu *
 575

<210> 55
 <211> 578
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37s

<400> 55
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 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
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 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser Leu Thr Val
 65 70 75 80
 Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn Ile Asn Leu
 85 90 95
 Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu Thr Val Ala
 100 105 110
 Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr Met Gln Ser
 115 120 125
 Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile Ala Thr Gln
 130 135 140
 Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln Thr Ser Gly
 145 150 155 160
 Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr Ala Ser Pro
 165 170 175
 Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu Lys Glu Pro
 180 185 190
 Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly Ala Pro Leu
 195 200 205
 His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr Gly Pro Gly
 210 215 220
 Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr Gly Ala Leu
 225 230 235 240
 Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala Gly Gly Leu
 245 250 255
 Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val Ser Tyr Pro
 260 265 270

Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln Gly Pro Leu
275 280 285
Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn Lys Gly Leu
290 295 300
Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu Val Asn Leu
305 310 315 320
Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile Ala Ile Asn
325 330 335
Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro Asn Thr Asn
340 345 350
Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp Ser Asn Ile
355 360 365
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
370 375 380
Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr Leu Trp Thr
385 390 395 400
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
405 410 415
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
420 425 430
Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
435 440 445
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
450 455 460
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
465 470 475 480
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
485 490 495
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
500 505 510
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
515 520 525
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
530 535 540
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
545 550 555 560
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
565 570 575
Gln Glu

<210> 56

<211> 1132

<212> DNA

<213> Artificial Sequence

<220>

<223> Ad37s/Ad5k fiber

<221> CDS

<222> (16)...(1116)

<221> misc_feature

<222> 1125

<223> n = A,T,C or G

<400> 56

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Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn	
1 5 10	
ccc gtc tac ccc tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc	99
Pro Val Tyr Pro Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu	
15 20 25	
act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg	147
Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly	
30 35 40	
gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat	195
Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp	
45 50 55 60	
gta tcc ctc aag gtg gga ggt ggt ctc act ttg caa gat gga agc cta	243
Val Ser Leu Lys Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu	
65 70 75	
act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt	291
Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu	
80 85 90	
gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt	339
Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser	
95 100 105	
tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg	387
Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala	
110 115 120	
ggg tta aaa gat tta att ggc aaa ctt gtg gtt tta aca gga aaa gga	435
Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly	
125 130 135 140	
ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att	483
Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile	
145 150 155	
ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac aat gat gga	531
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly	
160 165 170	
tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc	579
Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr	
175 180 185	
aca cca gct cca tct cct aac tgt aga cta aat gca gag aaa gat gct	627
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala	
190 195 200	
aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata ctt gct aca	675
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr	
205 210 215 220	

gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca 723
 Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
 225 230 235

gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg cta 771
 Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
 240 245 250

cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga 819
 Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
 255 260 265

gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct 867
 Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
 270 275 280

aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac 915
 Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
 285 290 295 300

att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca 963
 Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
 305 310 315

cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act cca 1011
 Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
 320 325 330

agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac 1059
 Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
 335 340 345

att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc 1107
 Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
 350 355 360

caa gaa taa agaagcggn c gctcga 1132
 Gln Glu *
 365

<210> 57

<211> 366

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad37s/Ad5k

<400> 57

Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys

50		55		60	
Val Gly Gly Gly Leu Thr	Leu Gln Asp Gly Ser	Leu Thr Val Asn Pro			
65	70	75	80		
Lys Ala Pro Leu Gln Val	Asn Thr Asp Lys Lys	Leu Glu Leu Ala Tyr			
	85	90	95		
Asp Asn Pro Phe Glu Ser	Ser Ala Asn Lys Leu	Ser Leu Lys Val Gly			
	100	105	110		
His Gly Leu Lys Val Leu	Asp Glu Lys Ser Ala	Ala Gly Leu Lys Asp			
	115	120	125		
Leu Ile Gly Lys Leu Val	Val Leu Thr Gly Lys	Gly Ile Gly Thr Glu			
	130	135	140		
Asn Leu Glu Asn Thr Asp	Gly Ser Ser Arg Gly	Ile Gly Ile Asn Val			
145	150	155	160		
Arg Ala Arg Glu Gly Leu	Thr Phe Asp Asn Asp	Gly Tyr Leu Val Ala			
	165	170	175		
Trp Asn Pro Lys Tyr Asp	Thr Arg Thr Leu Trp	Thr Thr Pro Ala Pro			
	180	185	190		
Ser Pro Asn Cys Arg Leu	Asn Ala Glu Lys Asp	Ala Lys Leu Thr Leu			
	195	200	205		
Val Leu Thr Lys Cys Gly	Ser Gln Ile Leu Ala	Thr Val Ser Val Leu			
	210	215	220		
Ala Val Lys Gly Ser Leu	Ala Pro Ile Ser Gly	Thr Val Gln Ser Ala			
225	230	235	240		
His Leu Ile Ile Arg Phe	Asp Glu Asn Gly Val	Leu Leu Asn Asn Ser			
	245	250	255		
Phe Leu Asp Pro Glu Tyr	Trp Asn Phe Arg Asn	Gly Asp Leu Thr Glu			
	260	265	270		
Gly Thr Ala Tyr Thr Asn	Ala Val Gly Phe Met	Pro Asn Leu Ser Ala			
	275	280	285		
Tyr Pro Lys Ser His Gly	Lys Thr Ala Lys Ser	Asn Ile Val Ser Gln			
	290	295	300		
Val Tyr Leu Asn Gly Asp	Lys Thr Lys Pro Val	Thr Leu Thr Ile Thr			
305	310	315	320		
Leu Asn Gly Thr Gln Glu	Thr Gly Asp Thr Thr	Pro Ser Ala Tyr Ser			
	325	330	335		
Met Ser Phe Ser Trp Asp	Trp Ser Gly His Asn	Tyr Ile Asn Glu Ile			
	340	345	350		
Phe Ala Thr Ser Ser Tyr	Thr Phe Ser Tyr Ile	Ala Gln Glu			
	355	360	365		

<210> 58
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad37 third repeat

<400> 58
Gly Ser Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp
1 5 10 15

<210> 59
 <211> 14
 <212> PRT

<213> Artificial Sequence

<220>

<223> Ad8 last repeat

<400> 59

Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asp Asn
1 5 10

<210> 60

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad9 last repeat

<400> 60

Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asn Asp
1 5 10

<210> 61

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad15 last repeat

<400> 61

Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Glu Ala
1 5 10

<210> 62

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Penton region

<400> 62

His Ala Ile Arg Gly Asp Thr Phe
1 5

<210> 63

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Penton amino acid replacement

<400> 63
Ser Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Ser
1 5 10 15

<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Fiber protein conserved sequence

<400> 64
Thr Trp Leu Thr
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<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> HSP binding motif

<400> 65
Lys Lys Thr Lys
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<210> 66
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad8 third repeat

<400> 66
Gly Lys Leu Thr Val Asn Thr Glu Pro Pro Leu His Leu Thr Asn Asn
1 5 10 15

<210> 67
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad9 third repeat

<400> 67
Gly Lys Leu Thr Val Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn
1 5 10 15

<210> 68
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 third repeat

<400> 68
Gly Asn Leu Thr Val Asn Thr Glu Pro Pro Leu Gln Leu Thr Asn Asn
1 5 10 15

<210> 69
<211> 3929
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector pCR2.1

<400> 69
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tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 180
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